VISA strains), with no totally vancomycin-resistant (VRSA) strains. All of phenotypic MRSA isolates, except of one, were positive for PBP2a.

Conclusion: The study concludes that *S. aureus* is the most prevalent pathogen causing bacteremia in leukemia patients, with MRSA variety comprising the majority of these strains. Also, phenotypic method for MRSA detection can be performed using either of Methicillin, Oxacillin, or Cefoxitin with same results, with a non-significant statistical difference between the phenotypic method and the genotypic method- via the PBP2a detection.

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Prevalence and risk factors for intestinal colonization with vancomycin resistant enterococci among patients admitted to intensive care units of a large teaching hospital in Southern India

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Background: Vancomycin Resistant Enterococci (VRE) emerged as one of the major nosocomial pathogen across the globe. Gut colonisation rate with VRE is higher in patients admitted to ICUs due to high antibiotic pressure. VRE colonisation increases the risk of developing infection up to 5-10 folds. The aim of this study was to determine the rates of VRE colonization among patients admitted in two of the ICUs i.e. Medical Intensive Care Unit (MICU) and Pediatric Intensive Care Unit (PICU) and to assess the various risk factors which are associated with VRE colonization.

Methods & Materials: Rectal swabs were collected after 48 hours of ICU admission from a total of 302 and 198 patients from MICU and PICU respectively. Additionally samples were collected every 48 hours from 32 patients admitted in MICU and 19 patients in PICU whose initial VRE colonization was negative. The samples were inoculated on to Bile Esculin Sodium azide Agar (BEA) with 6 mg/ml of vancomycin. Growth on this medium were identified by standard biochemical test and Minimum Inhibitory Concentration (MIC) of vancomycin and teicoplanin was detected by Agar dilution method. Resistance genes for vancomycin were detected by PCR. Risk factors were assessed by logistic regression analysis. The patients were followed up to determine VRE infection rates

Results: The rates of VRE colonization in patients admitted to MICU was significantly higher (29%) than those in PICU (19%). Majority of the isolates were *Enterococcus faecalis* (62.6%) followed by *Enterococcus faecium* (38.4%). All the VRE isolates were positive for *van*A gene. Younger age, increased duration of hospital stay, consumption of ceftriaxone and vancomycin were found to be significantly associated with VRE colonization in MICU, while in PICU, only vancomycin usage was the significant risk factor. Among VRE colonized patients, six (4.7%) acquired VRE infection.

Conclusion: The VRE colonization rates in our ICUs were comparable to other hospitals worldwide. Strict adherence to hand hygiene and education of health care workers is necessary to minimize the nosocomial transmission of this organism.

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A study of 24 patients with colistin resistant gram negative isolates in a tertiary care hospital in South India

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Background: As the use of colistin to treat carbapenem resistant gram negative infections increases, colistin resistance is being increasingly reported in Indian hospitals.

Methods & Materials: Retrospective chart review of clinical data from patients with colistin resistant isolates (MIC > 2). Clinical profile, outcome and antibiotic combinations that were used to treat colistin resistant infection were analysed.

Results: Twenty four colistin resistant isolates were reported over 18 months (Jan 2014–June 2015). The mean age of the patients was 58.33; average length of stay was 36.37 days. Previous hospitalisation within 3 months was noted in all 24 patients. An invasive device was used in 22(91.67%) patients. Urine was the commonest site of infection=8(33%), followed by blood= 6(25%), respiratory=5(20.8%), pus=4(16.67%) and other (CSF)=1(4.17%). Commonest organism was Klebsiella, n = 21(87.5%). Antibiotics that were used in their current admission prior to isolating a colistin resistant organism were: colistin in 15 patients(62.5%), carbapenem in 19(79.17%), BL-BLI in 9(37.5%), tigecycline in 12(50%). 16(66.6%) were considered to have true infection while 8 (33.3%) were considered as colonisation and were not treated. Sensitivity of these isolates to other drugs tested were – tigecycline 18/24(75%), chloramphenicol 15/24(62.5%), amikacin 7/24(29.17%), cotrimoxazole 3/24(12.5%). Fosfomycin was tested in 4 isolates only and was sensitive in all. Antibiotic that were used for treatment were combinations of tigecycline, chloramphenicol, fosfomycin, amikacin, ciprofloxacin, cotrimoxazole and sulbactam. Among 16 patients with true infection, 4(25%) improved, 9(56.25%) expired and 3(18.75%) were transferred to other centers in poor condition at patient's request. Among 8 patients who were considered to have colonisation, there were no deaths and 7(87.5%) improved. Among the 6 bacteremic cases, 5 patients expired and 1 improved. Among the non-bacteremic patients with true infections 4/10(40%) expired. Bacteremic patients had a significantly higher risk of death compared to all non-bacteremic patients (p = 0.014) though not significantly in non-bacteremic infections after exclusion of colonization (p = 0.145).

Conclusion: Colistin resistance among Gram negative bacteria, especially Klebsiella, is emerging in Indian hospitals and carries a

high crude mortality. Prolonged hospitalization (36 days on average), use of invasive devices and prior colistin exposure may be risk factors. Tigecycline, chloramphenicol and fosfomycin may be options for combination therapy.

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Genotypic and phenotypic characterization of antimicrobial resistance in staphyloccoccus aureus strains isolated from wound infections in Mardin, Southeastern Turkey

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Background: Nosocomial and community-acquired infections caused by *Staphylococcus aureus* are still a worldwide growing problem. The aim of this study was to evaluate the phenotypic and genotypic antimicrobial susceptibility patterns of *S.aureus* isolated from wound samples of Turkish patients living in Mardin, Southeastern Turkey.

Methods & Materials: A total of 220 clinical wound samples, collected between December 2012 - August 2013 were used in this study. The identification of *S. aureus* was made by conventional methods. The antimicrobial susceptibility of *S. aureus* strains to eleven antimicrobial agents was performed by the disk diffusion method and the results were evaluated according to EUCAST 2014 guidline. Additionnaly, DNA was extracted from the wound samples using the High Pure PCR template preparation kit. Eleven genes indicating the genotypic resistance to oxacillin (mecA), gentamicin (aac(6′)-aph(2′), aph(3′)-IIIa, ant(4′)-Ia), erythromycin (ermA, ermB, ermC, and msrA), tetracyclin (tetK, tetM) and penicillin (blaZ) were amplified using multiplex PCR and were visualized using gel imaging.

Results: *S.aureus* was isolated from 112 (50,91%) of 220 wound samples. The phenotypic resistance rates of *S.aureus* was found 45.54% (51 strains) for penicilin G, 41.07% (46 strains) for ampicillin, 33.04% (37 strains) for tetracycline, 26.79% (30 strains) for erythromycin, 5.36% (6 strains) for trimethoprim-sulfamethaxasol, 4.46% (5 strains) for oxacilline, 0.89% (1 strain) for amoxycillin-clavulanic acid and 0.89% (1 strain) for enrofloxacin All isolates were found to be susceptible to gentamicin, vancomycin and teicoplanin. None of isolates showed an aminoglycoside resistance genotypically. The number and rates of MSSA and MRSA carrying antibiotic resistance genes were 19 (16,96%) and 32 (28,57%) for blaZ, 9 (8,04%)and 17 (15,18%) for tetK, 6 (5,36%)and 14 (12,5%) for ermC, 2 (1,79%)and 7 (6,25%) for tetM, 0 (0%)and 5 (4,46%) for mecA, 2 (1,79%)and 4 (3,57%) for ermA, 1 (0,89%)and 2 (1,79%) for both tetK and tetM respectively.

Conclusion: The data obtained facilitate the nationwide surveillance of the antimicrobial resistance gene profiles of S.aureus for accurate treatment of patients and to control the dissemination of resistance genes

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Frequent resistant gram negative rod stool colonization among patients admitted with acute febrile illness in Pune, India

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Background: Antimicrobial resistance is increasing worldwide, including in India. There is a concern that unfettered antibiotic use may be associated with increasing antimicrobial resistance. Surveillance for antimicrobial resistance may be accomplished by evaluating for stool colonization of drug resistant organisms.

Methods & Materials: Patients >12 years of age admitted to adult medicine wards at BJ Medical College - Sassoon General Hospital, in Pune, India with >1 day of fever were enrolled into a prospective cohort between July 2013 and September 2015. A perianal swab sample was collected on the day of enrollment and on day 3–5 of hospitalization and stored at −80 °C pending processing. Samples were aspirated onto peptone broth impregnated with ceftriaxone and vancomycin, incubated, and then plated onto MacConkey and blood agar. Identification and drug susceptibility testing was performed on isolates using a Phoenix system (Becton Dickinson).

Results: Perianal swabs were collected on 314 patients at the time of enrollment. Follow up swabs were collected on 181 patients – 158 on day 3, 22 on day 4, and 1 on day 5. There was growth of resistant gram negative rods (GNR) in 60 (19%) patients. In 9 (2.9%) of patients, there was growth of GNR resistant to imipenem. Seventeen patients who were not colonized with resistant GNR upon enrollment were colonized at the time of follow up. Inpatient use of cephalosporins was associated with acquisition of colonization with resistant GNR, odds ratio 3.68, 95% confidence interval 1.02–13.31.

Conclusion: Perianal colonization with resistant gram negative rods is common among patients admitted to medicine wards in Pune, India. The association of acquisition of drug resistance during a brief hospitalization with prescription of cephalosporins highlights the need for improved antimicrobial stewardship.

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